

AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (currently amended) A method for identifying an ~~agent that has an inhibitory effect on an~~ inhibitor of the complex-formation of an ARE-containing mRNA and an HuR (Hu-Antigen R) protein comprising:
 - (a) providing a soluble form of a HuR protein selected from the group of proteins consisting of the amino acid sequences set forth in SEQ ID NO:3 or SEQ ID NO:4, ~~with the proviso that a full-length HuR-glutathione-S-transferase fusion protein is excluded,~~
 - (b) providing an ARE-containing mRNA,
 - (c) providing a candidate ~~compound~~ inhibitor, wherein at least one of (a), (b) and (c) is labeled,
 - (d) mixing the HuR protein of step (a) and the ARE-containing mRNA of step (b)
 - (i) in the presence of the candidate inhibitor of step (c) and
 - (ii) in the absence of the candidate inhibitor of step (c)for a sufficient period of time so that the HuR protein of step (a) and the ARE-containing mRNA of step (b) can form a complex,
 - (e) detecting the amount of complexes formed in step (d) and/or detect the non-complexed mRNA/protein species,
 - (f) comparing the amount of complexes formed in step (d)(ii) and/or with the non-complexed mRNA/protein species formed in step (d)(i) found in the presence and in the absence of (e), and
 - (g) ~~choosing an agent which has an influence on the complex formation detected in step (f)~~ identifying a candidate inhibitor that inhibits complex formation between the ARE-containing mRNA and the HuR protein.
2. (original) The method of claim 1 characterized in that the HuR protein is provided as a homogenous solution.
3. (previously presented) The method of claim 1 characterized in that HuR is a soluble form of a recombinant full-length protein or a variant or mutant of a soluble form of a full-length protein.
4. (previously presented) The method of claim 1 characterized in that the mRNA fragment is fluorescently labeled.

5. (currently amended) The method of claim 1 characterized in that the ~~detection method~~ is candidate inhibitor is identified by use of a fluorescence spectroscopic method selected from the group consisting of Single Molecule Spectroscopy, Fluorescence Correlation Spectroscopy, Fluorescence Intensity Distribution Analysis, Steady-State Fluorescence Intensity, Fluorescence Anisotropy and Energy Transfer.
6. (withdrawn from consideration) A screening assay (kit) for identifying an agent that has an inhibitory effect on the complex-formation of an ARE-containing mRNA and an HuR protein comprising as a main component
 - (a) a soluble form of a HuR protein, with the proviso that a full-length HuR–glutathione-S-transferase fusion protein is excluded,
 - (b) an ARE-containing mRNA, and
 - (c) optionally means for detection of the amount of complexes formed between said HuR protein and said ARE-containing mRNA and/or for detection of non-complexed mRNA/protein species.
7. (withdrawn from consideration) A pharmaceutical composition comprising an agent identified by a method according to claim 1 in association with at least one pharmaceutical excipient.
8. (withdrawn from consideration) Use of a pharmaceutical composition according to claim 7, for the treatment of a disorder having an etiology associated with the production of a substance selected from the group consisting of cytokine, growth factor, proto-oncogene or a viral protein, preferably the agent is selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-8, GM-CSF, TNF- α , VEGF, AT-R1, Cox-2, c-fos and c-myc.
9. (withdrawn from consideration) A full-length HuR protein of SEQ ID NO:1 or SEQ ID NO:2, wherein the C-terminal amino acid in position 326 is esterified.
10. (withdrawn from consideration) An isolated RNA sequence motif which is the binding site for HuR.